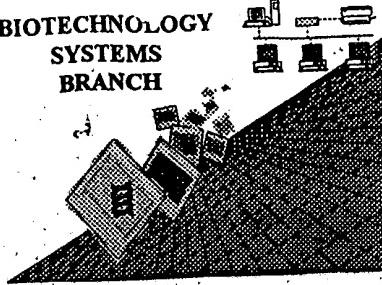


Ganskroft

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/236,995C  
Source: 1600 Rust  
Date Processed by STIC: 8/15/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE  
APPLICANT, WITH A NOTICE TO COMPLY or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A  
NOTICE TO COMPLY.  
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/236,998C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENCLISII "ALPHIA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic Acid Sequences The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino Acid Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
 (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
 <210> sequence id number  
 <400> sequence id number  
 000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

1636

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/236,995C

DATE: 08/15/2001  
TIME: 12:25:58

Input Set : A:\Polyadpl.app  
Output Set: N:\CRF3\08152001\I236995C.raw

PP, 2/3  
Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Mahajan, Pramod B.  
4 Zuo, Zhuang  
6 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and Its Uses  
8 <130> FILE REFERENCE: 5718-34, 035718-174234  
10 <140> CURRENT APPLICATION NUMBER: 09/236,995C  
11 <141> CURRENT FILING DATE: 1999-01-26  
13 <150> PRIOR APPLICATION NUMBER: 60/072,785  
14 <151> PRIOR FILING DATE: 1998-01-27  
16 <160> NUMBER OF SEQ ID NOS: 5  
18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

289 <210> SEQ ID NO: 2  
290 <211> LENGTH: 982  
291 <212> TYPE: PRT  
292 <213> ORGANISM: Zea mays  
294 <400> SEQUENCE: 2  
295 Met Ala Ala Pro Pro Lys Ala Trp Lys Ala Glu Tyr Ala Lys Ser Gly  
296 1 5 10 15  
297 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu  
298 20 25 30  
299 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro  
300 35 40 45  
301 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys  
302 50 55 60  
303 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln  
304 65 70 75 80  
305 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser  
306 85 90 95  
307 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala  
308 100 105 110  
309 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val  
310 115 120 125  
311 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp  
312 130 135 140  
313 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu  
314 145 150 155 160  
315 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met  
316 165 170 175  
317 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly  
318 180 185 190  
319 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala  
320 195 200 205  
321 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln  
322 210 215 220

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/236,995C

DATE: 08/15/2001  
TIME: 12:25:58

Input Set : A:\Polyadpl.app  
Output Set: N:\CRF3\08152001\I236995C.raw

323 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu  
 324 225 230 235 240  
 325 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu  
 326 245 250 255  
 327 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn  
 328 260 265 270  
 329 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala  
 330 275 280 285  
 331 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn  
 332 290 295 300  
 333 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser  
 334 305 310 315 320  
 335 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys  
 336 325 330 335  
 337 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys  
 338 340 345 350  
 339 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro  
 340 355 360 365  
 341 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu  
 342 370 375 380  
 343 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln  
 344 385 390 395 400  
 345 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly  
 346 405 410 415  
 347 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala  
 348 420 425 430  
 349 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg  
 350 435 440 445  
 351 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys  
 352 450 455 460  
 353 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu  
 354 465 470 475 480  
 E--> 355 Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala  
 356 485 490 495  
 E--> 357 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa  
 358 500 505 510  
 E--> 359 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa  
 360 515 520 525  
 E--> 361 His Xaa Val Cys Thr Gly Tyr Val Leu Gln Ile Ile Glu Gln Asp  
 362 530 535 540  
 363 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser  
 364 545 550 555 560  
 365 Glu Lys Ile Gly Gly Gln Lys Leu Glu Met Ser Lys Thr Glu Ala  
 366 565 570 575  
 367 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp  
 368 580 585 590  
 369 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe  
 370 595 600 605  
 371 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys

All item 9  
 on Env  
 summary  
 sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/236,995C

DATE: 08/15/2001  
TIME: 12:25:58

Input Set : A:\Polyadpl.app  
Output Set: N:\CRF3\08152001\I236995C.raw

372	610	615	620
373	Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu		
374	625	630	640
375	Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu		
376	645	650	655
E--> 377	Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa		
378	660	665	670
E--> 379	Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe		
380	675	680	685
E--> 381	Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu		
382	690	695	700
E--> 383	Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu		
384	705	710	720
385	Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu		
386	725	730	735
387	Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp		
388	740	745	750
389	Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys		
390	755	760	765
391	Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu		
392	770	775	780
393	Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu		
394	785	790	800
395	Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys		
396	805	810	815
397	Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His		
398	820	825	830
399	Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg		
400	835	840	845
401	Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly		
402	850	855	860
403	Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val		
404	865	870	875
405	Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu		
406	885	890	895
407	Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro		
408	900	905	910
409	Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu		
410	915	920	925
411	Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys		
412	930	935	940
413	Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr		
414	945	950	955
415	Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val		
416	965	970	975
417	Arg Phe His His Lys Arg		
418	980		

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/236,995C

DATE: 08/15/2001  
TIME: 12:25:59

Input Set : A:\Polyadp1.app  
Output Set: N:\CRF3\08152001\I236995C.raw

L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:355 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2  
M:340 Repeated in SeqNo=2